

FIG. 1A

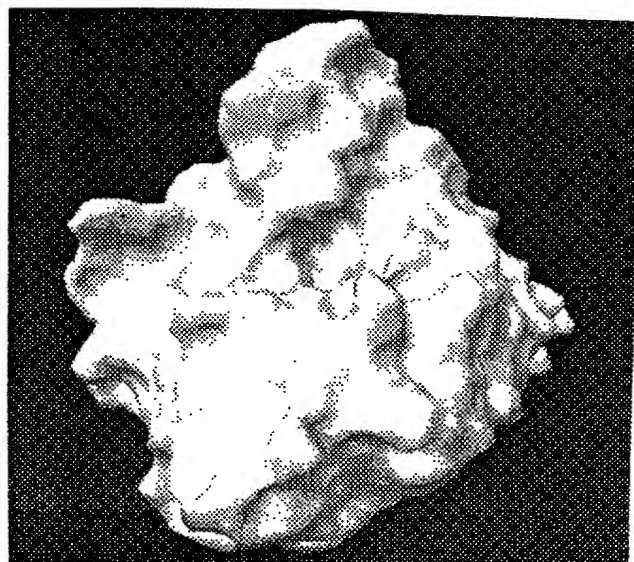


FIG. 1B

Fig. 2A

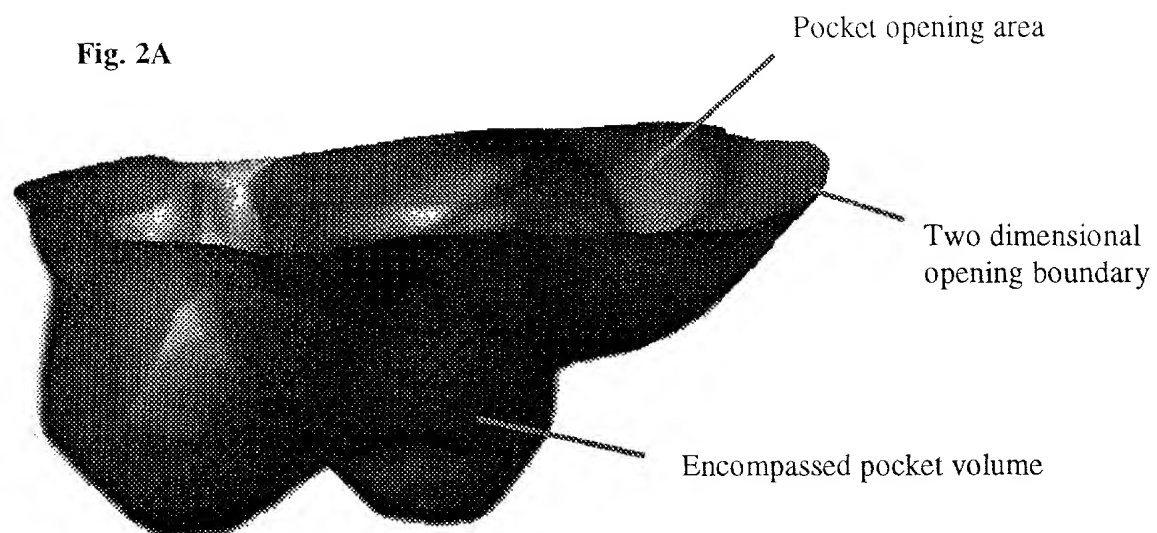
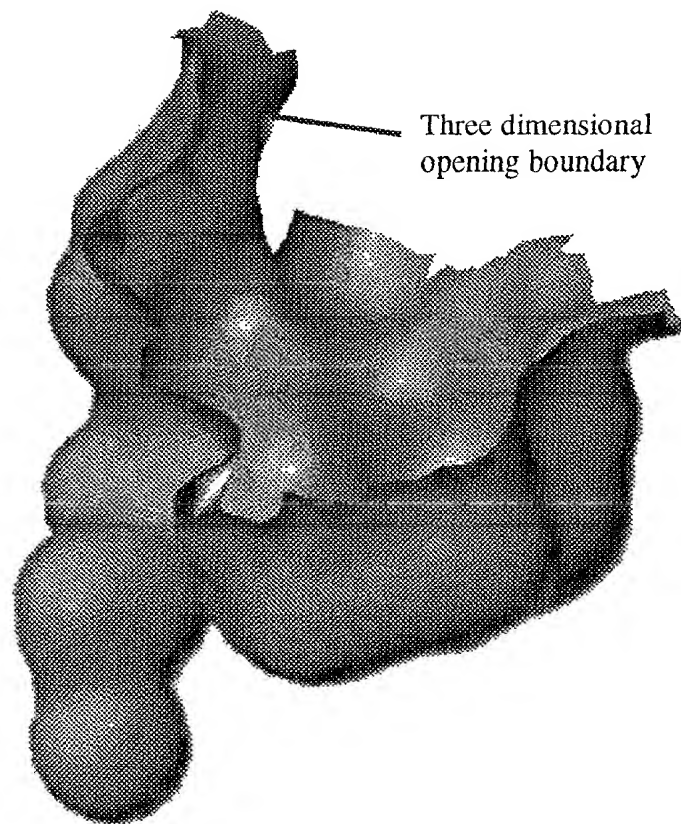


Fig. 2B



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Fig. 3A

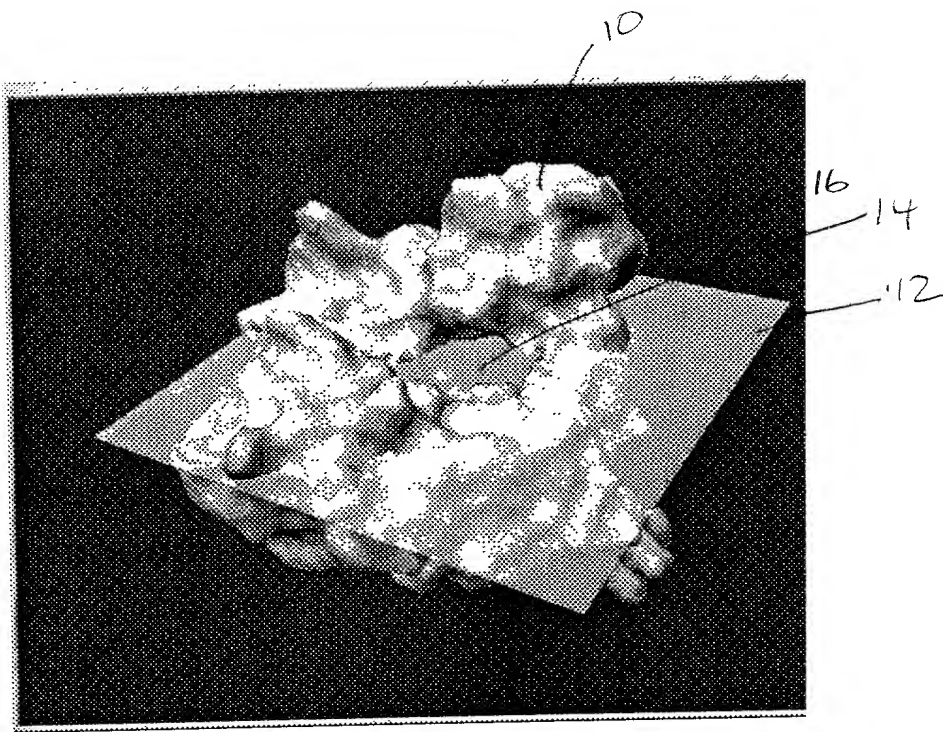


Fig. 3B

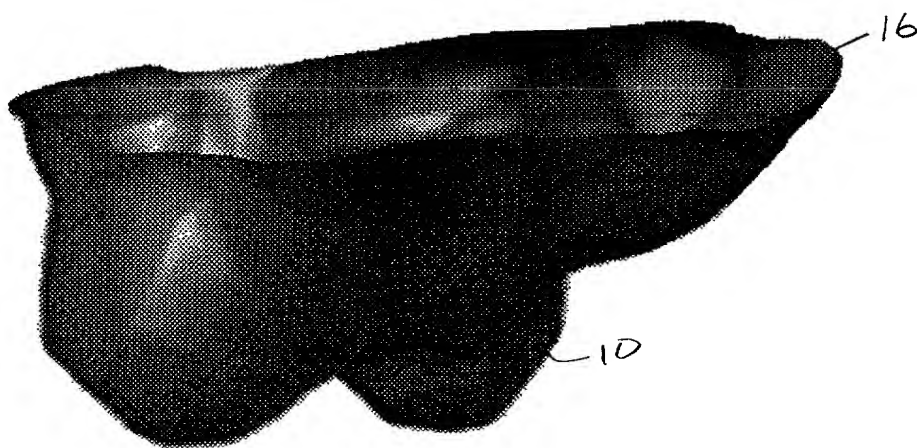


Fig. 4A

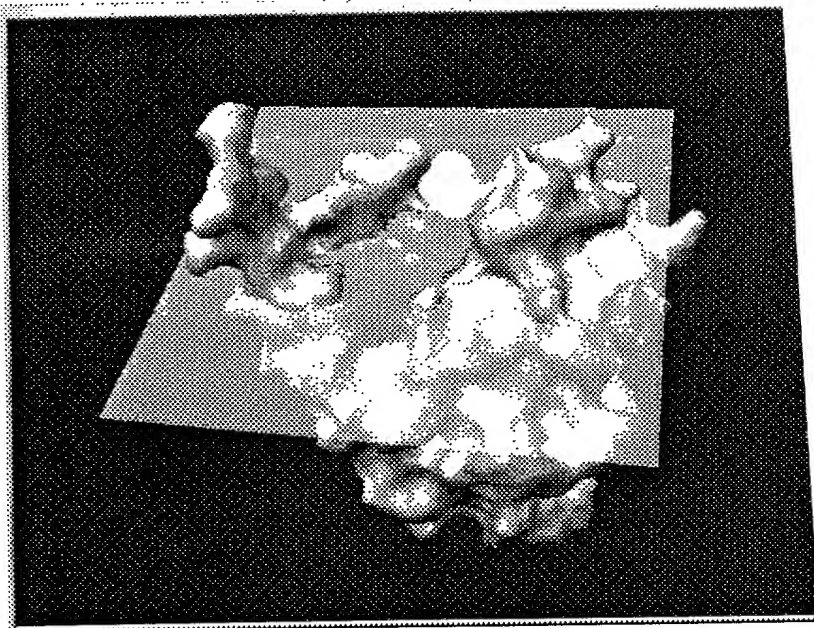
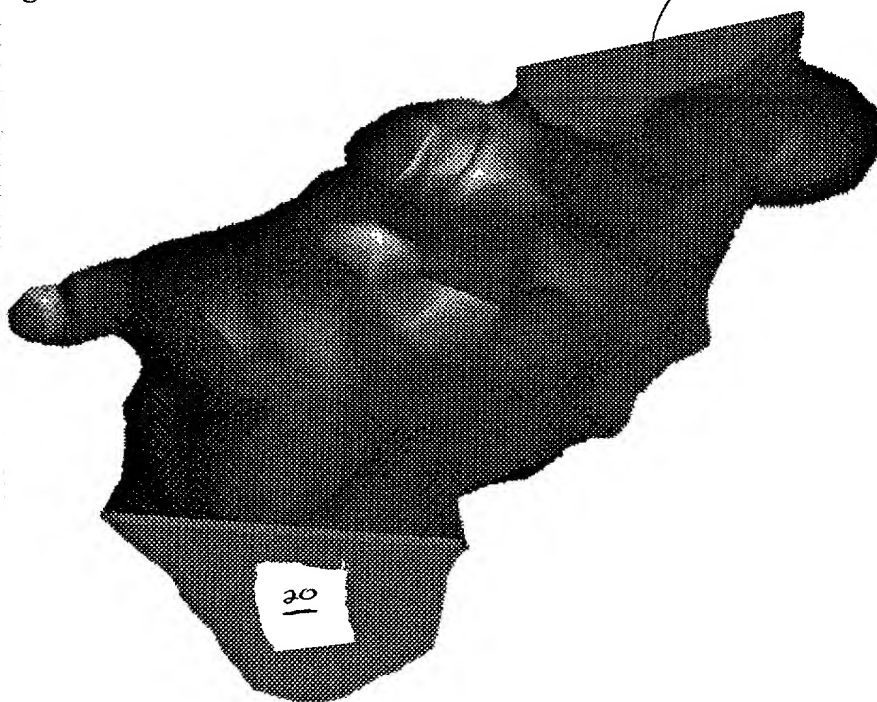


Fig. 4B



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Fig. 5A

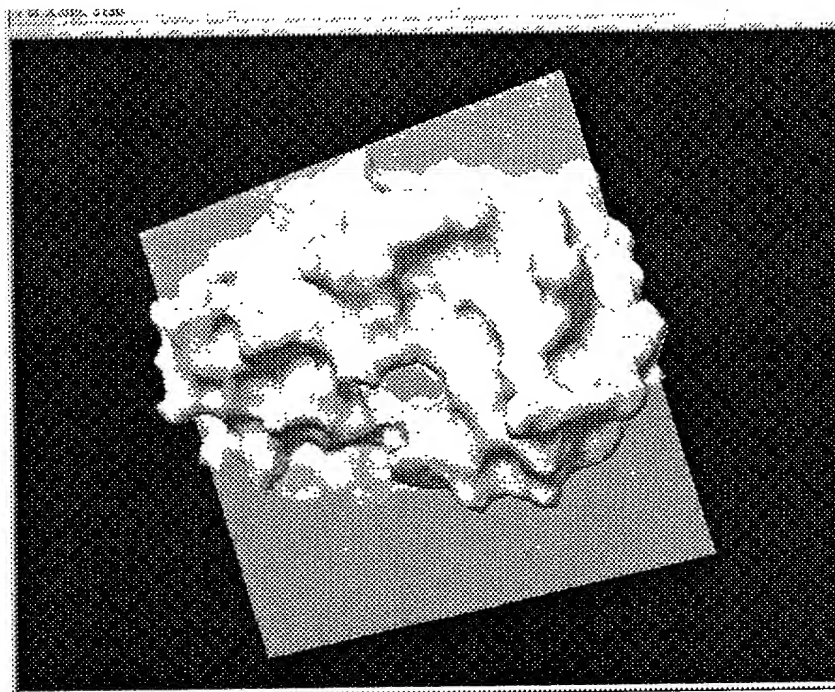


Fig. 5B

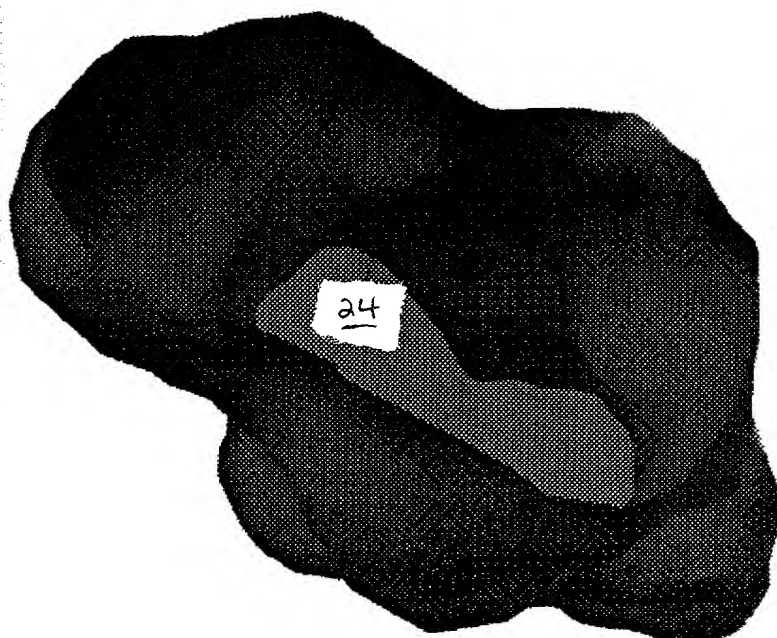


Fig. 6: HIV-1 Protease protein surface showing an actual ligand as determined by x-ray co-crystal structure and showing the pocket of highest volume as calculated by the method of this application

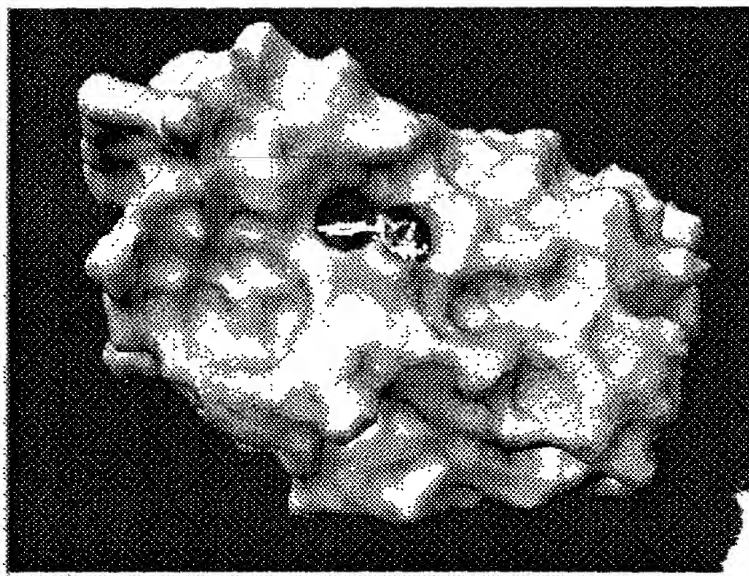


Fig. 7: Heat Shock Protein 90 surface showing an actual ligand as determined by x-ray co-crystal structure and showing the pocket of highest volume as calculated by the method of this application

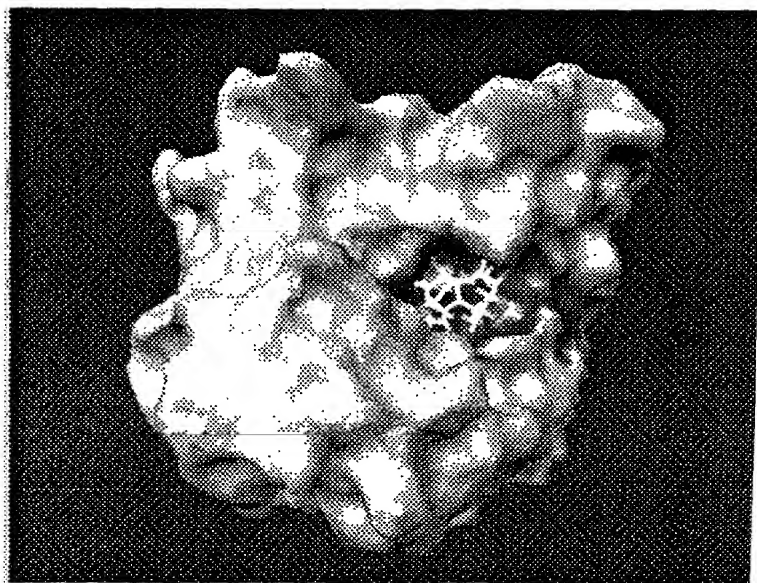


Fig. 8: Stromelysin protein surface showing an actual ligand as determined by x-ray co-crystal structure and showing the pocket of highest volume as calculated by the method of this application

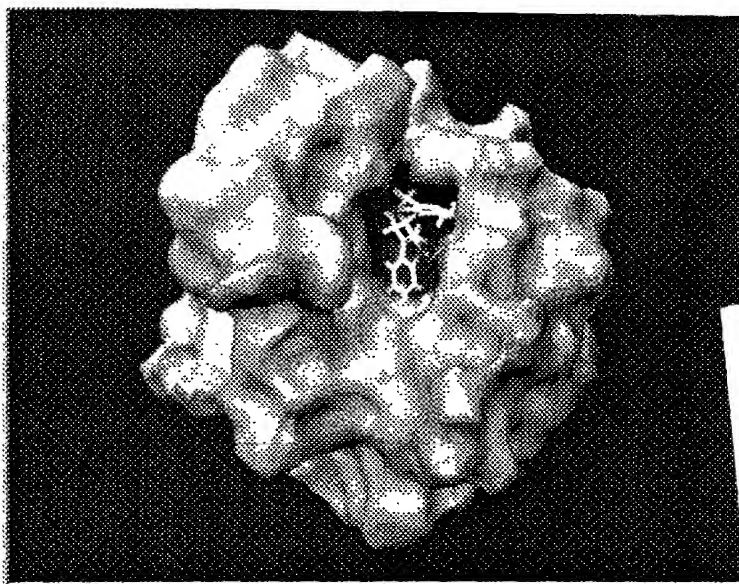


Fig. 9: Dihydrofolate Reductase protein surface showing an actual ligand as determined by x-ray co-crystal structure and showing the pocket of highest volume as calculated by the method of this application

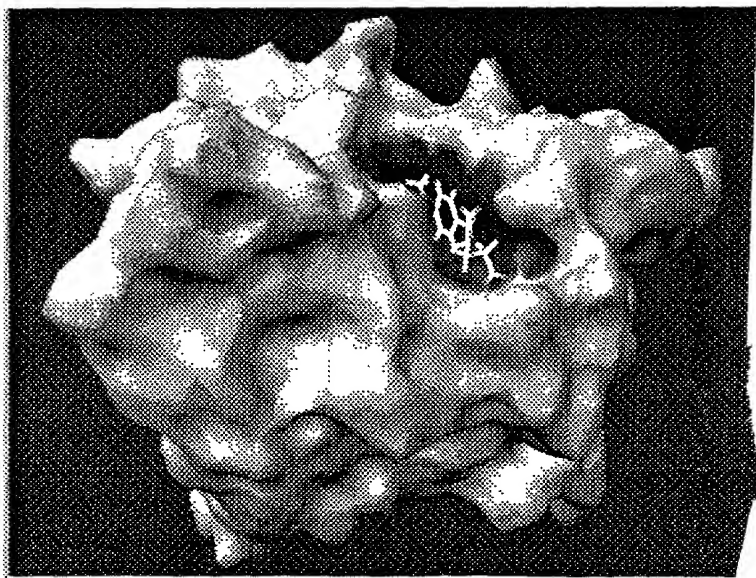
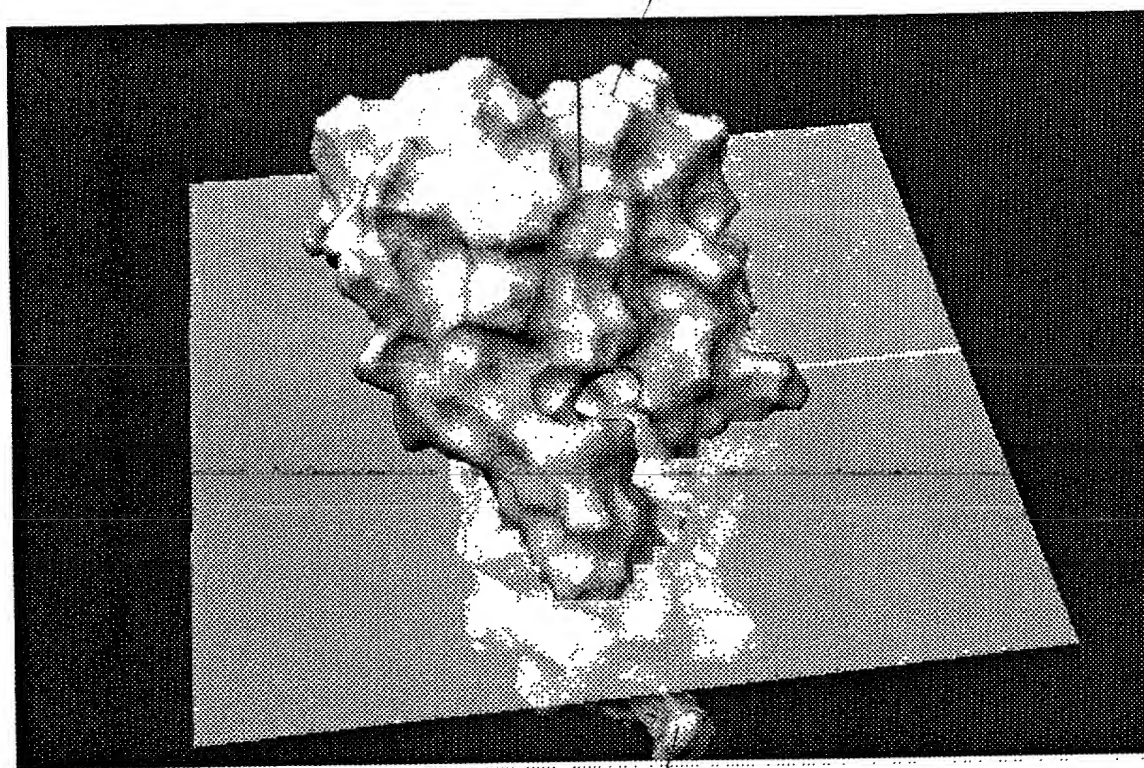


FIG. 10



STOP 30

S_{BOTTOM} 32

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FIG. 11

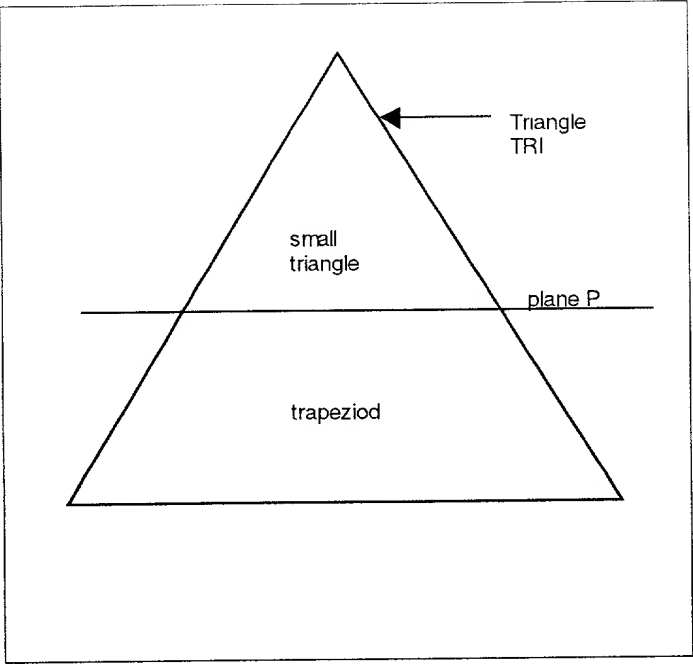


FIG. 12

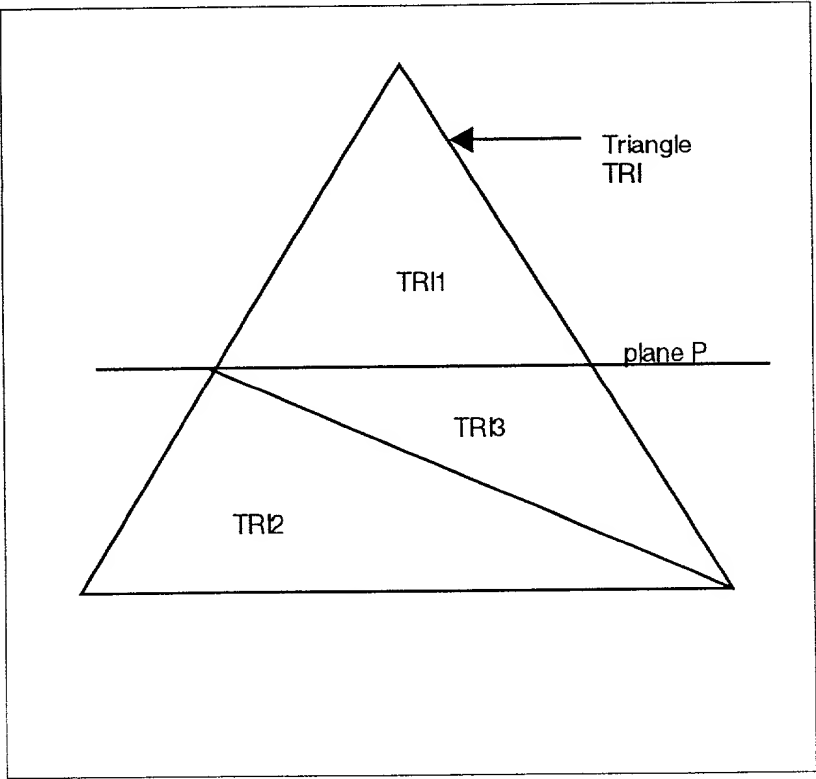
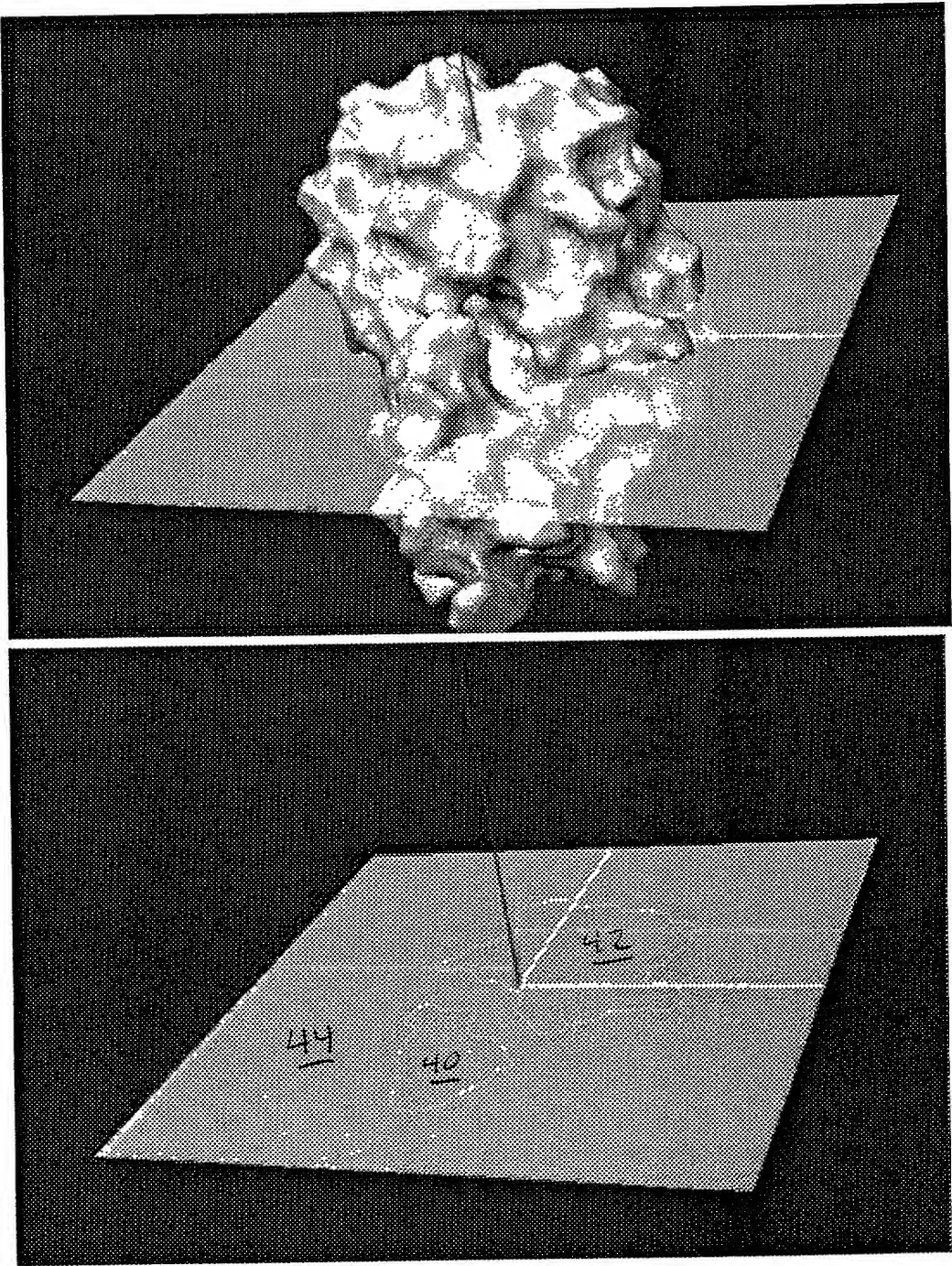


FIG. 13



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FIG. 14:

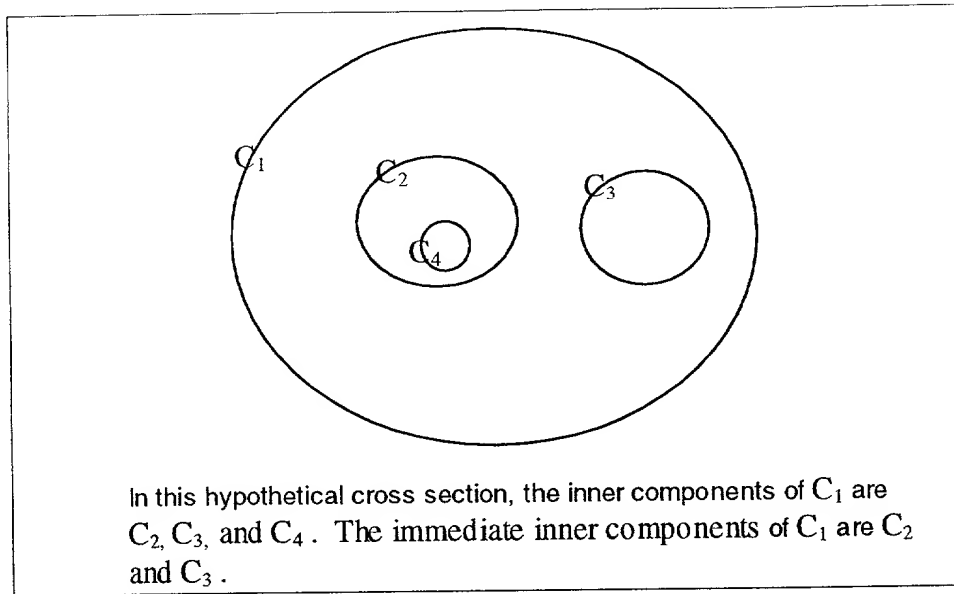
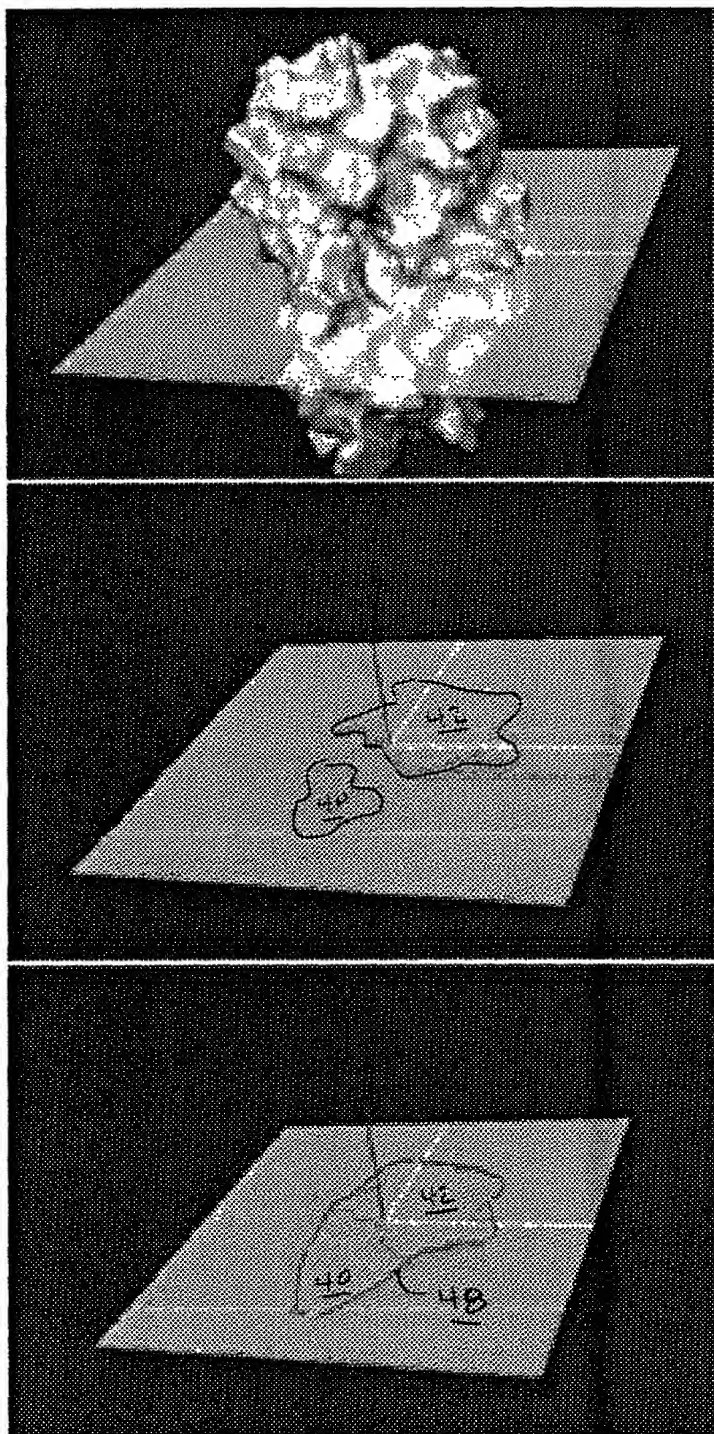


FIG. 15



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FIG. 16.

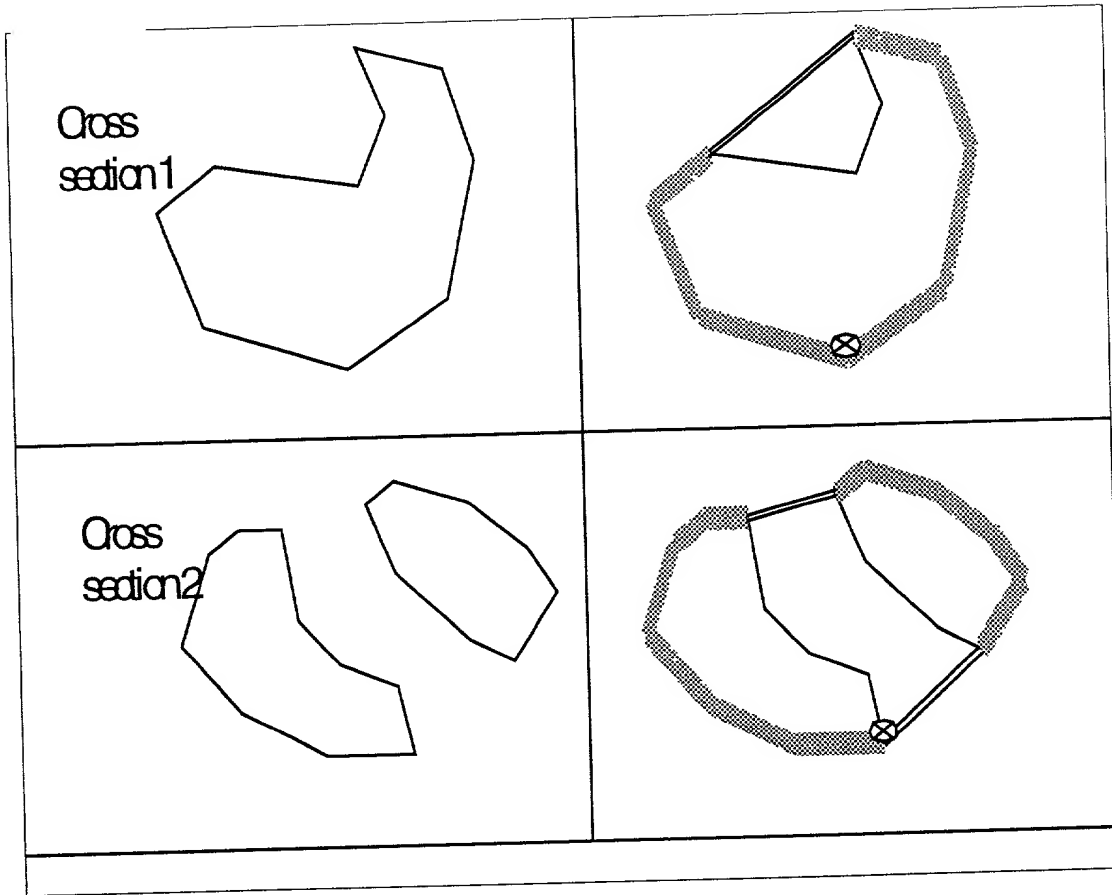


FIG. 17

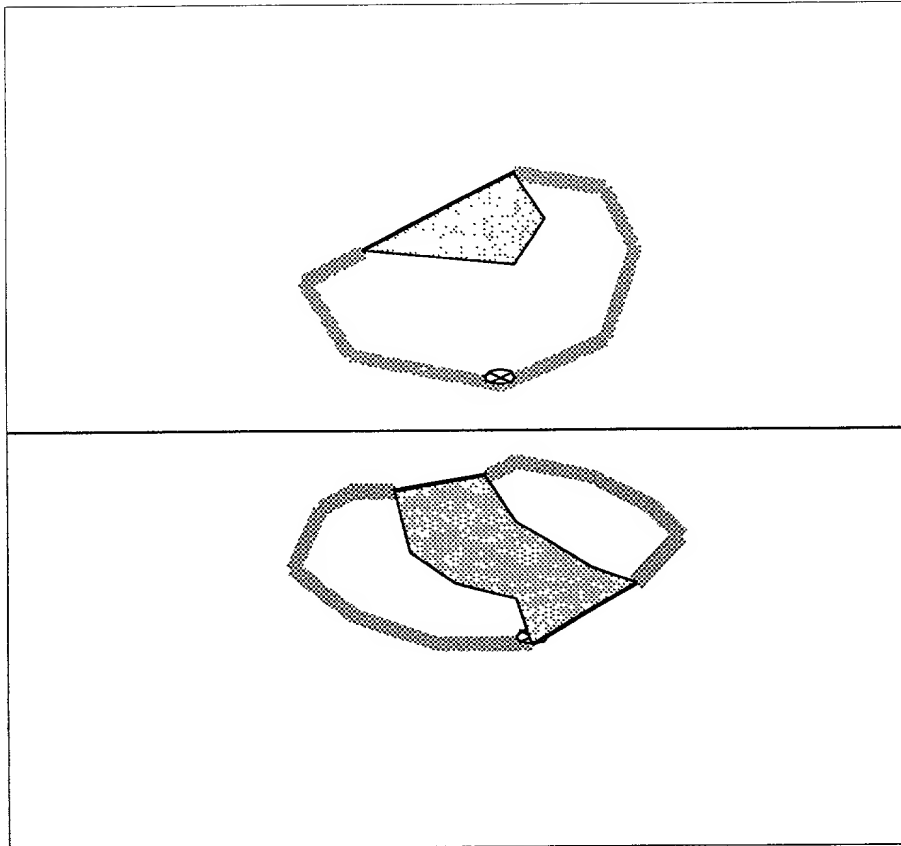


FIG. 18

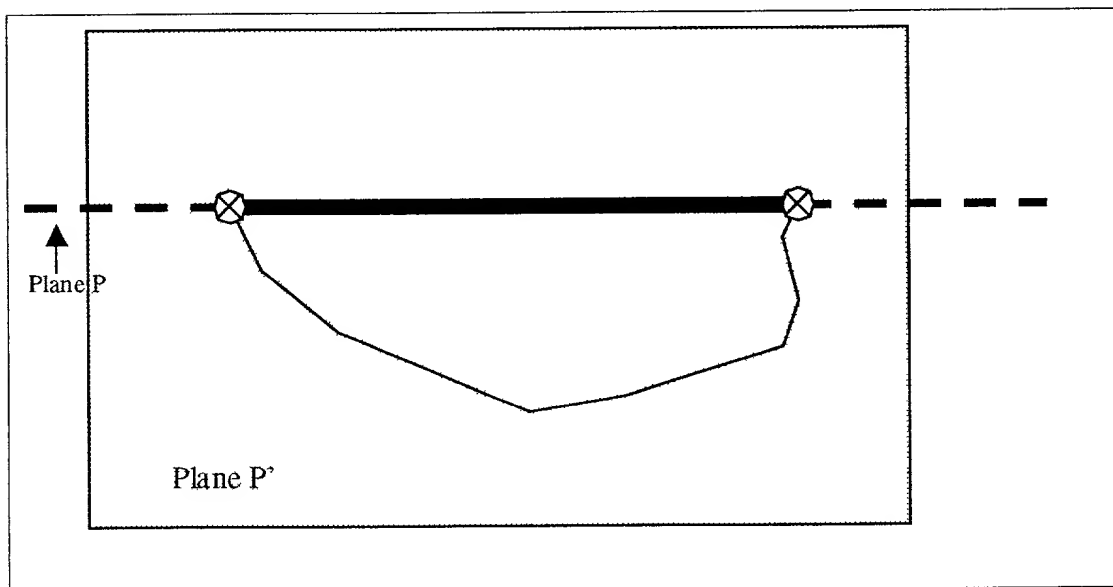
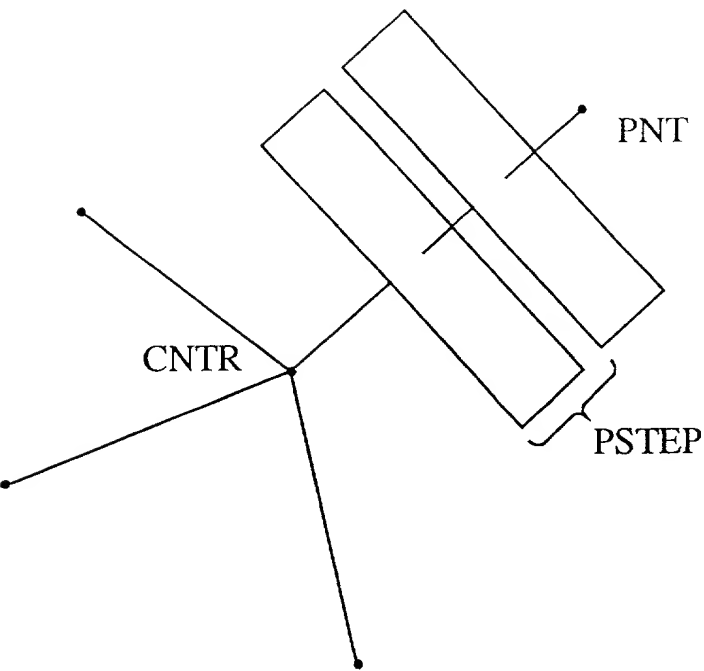


Figure 19:
Two plane slices shown for N = 4 (four points PNT distributed about a sphere)



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